CLAIMS

1. A computer-implemented method for displaying data comprising:

   a) providing an icon representative of a single data measurement;

   b) shading the icon with color, wherein color hue indicates directionality of change relative to a standard;

   c) adjusting color saturation in the shaded icon when the single data measurement is changed relative to the standard, wherein amount of color indicates degree of change relative to the standard; and

   d) displaying the icon generated by steps (a) through (c) singularly or with a plurality of icons generated by steps (a) through (c).

2. The method of claim 1, wherein the color shading of step (b) is red, green, or gray color.

3. The method of claim 1, wherein the data measurement is stored as a numeric value in a data source

4. The method of claim 3, wherein the data source is a database.

5. The method of claim 1, wherein the data measurement is selected from the group consisting of a biochemical profiling data measurement, a gene expression profiling data measurement, an histology data measurement, a phenotype data measurement, or a proteomics data measurement.

6. The method of claim 1, wherein the icon is representative of a single metabolite.

7. The method of claim 1, wherein the icon is representative of a single gene.

8. The method of claim 1, wherein the icon is representative of a single gene and all icons representative of genes pertaining to a single enzyme are displayed in a vertically stacked orientation.

9. The method of claim 8, wherein iconic placement in the stack is determined by directionality and magnitude of change as compared to a standard.

10. The method of claim 1, wherein icons representative of two or more data types are displayed simultaneously.

11. The method of claim 3, wherein the interaction between the data source and the iconic display is dynamic.

12. A computer-implemented method for displaying biological sample data, wherein the data are displayed in a biological context comprising:

   a) providing an icon representative of a single data measurement;

   b) shading the icon with color, wherein color hue indicates directionality of change relative to a standard;

   c) adjusting color saturation in the shaded icon when the single data measurement is changed relative to the standard, wherein amount of color indicates degree of change relative to the standard;

   d) selecting a biological context;

   e) displaying the biological context; and

   f) displaying the icon generated by steps (a) through (c) singularly or with a plurality of icons generated by steps (a) through (c) in a way that is representative of a relationship between the icon and the biological context.

13. The method of claim 12, wherein the color shading of step (b) is red, green, or gray color.

14. The method of claim 12, wherein the data measurement is stored as a numeric value in a data source.

15. The method of claim 14, wherein the data source is a database.

16. The method of claim 12, wherein the data measurement is selected from the group consisting of a biochemical profiling data measurement, a gene expression profiling data measurement, an histology data measurement, a phenotype data measurement, or a proteomics data measurement.

17. The method of claim 12, wherein the icon is representative of a single metabolite.

18. The method of claim 12, wherein the icon is representative of a single gene.

19. The method of claim 12, wherein the icon is representative of a single gene and all icons representative of genes pertaining to a single enzyme are displayed in a vertically stacked orientation.

20. The method of claim 19, wherein iconic placement in the stack is determined by directionality and magnitude of change as compared to a standard.

21. The method of claim 12, wherein icons representative of two or more data types are displayed simultaneously.

22. The method of claim 12, wherein the biological context is stored as alphanumeric values in a data source.

23. The method of claim 14, wherein the data source is a database.

24. The method of claim 12, wherein the biological context is represented as a graphical display.

25. The method of claim 24, wherein the graphical display type is selected from the group consisting of hierarchical, organic, circular, and orthogonal.

26. The method of claim 12, wherein the biological context is a biochemical network.

27. The method of claim 14, wherein the interaction between the data source and the iconic display is dynamic.

28. The method of claim 22, wherein the interaction between the data source and the display of the biological context is dynamic.

29. A computer-implemented method for supplying a biological context in which to display biological data comprising:

   a) providing at least one biological context stored as a set of alphanumeric values in a data source;

   b) providing at least one type of graphical display of the biological context, wherein the interaction between the data source and the graphical display is dynamic;

   c) selecting one biological context type for display;

   d) providing at least one icon representative of at least one biological data measurement;

   e) displaying the icon with the biological context in a way that is representative of a relationship between the icon and the biological context; and

   f) optionally, repeating steps (c) through (e).

30. The method of claim 29, wherein the data source is a database.

31. The method of claim 29, wherein the data measurement is selected from the group consisting of a biochemical profiling data measurement, a gene expression profiling data measurement, an histology data measurement, a phenotype data measurement, or a proteomics data measurement.

32. The method of claim 29, wherein the icon is representative of a single metabolite.

33. The method of claim 29, wherein the icon is representative of a single gene.

34. The method of claim 29, wherein the icon is representative of a single gene and all icons representative of genes pertaining to a single enzyme are displayed in a vertically stacked orientation.

35. The method of claim 34, wherein iconic placement in the stack is determined by directionality and magnitude of change as compared to a standard.

36. The method of claim 29, wherein icons representative of two or more data types are displayed simultaneously.

37. The method of claim 29, wherein the graphical display type is selected from the group consisting of hierarchical, organic, circular, and orthogonal.

38. The method of claim 29, wherein the biological context is a biochemical network.

39. A computer-implemented system for displaying data comprising:

    a) means for providing an icon representative of a single data measurement;

    b) means for shading the icon with color, wherein color hue indicates directionality of change relative to a standard;

    c) means for adjusting color saturation in the shaded icon when the single data measurement is changed relative to the standard, wherein amount of color indicates degree of change relative to the standard; and

    d) means for displaying the icon generated by steps (a) through (c) singularly or with a plurality of icons generated by steps (a) through (c).

40. The system of claim 39, wherein the color shading of step (b) is red, green, or gray color.

41. The system of claim 39, wherein the data measurement is stored as a numeric value in a data source.

42. The system of claim 41, wherein the data source is a database.

43. The system of claim 39, wherein the data measurement is selected from the group consisting of a biochemical profiling data measurement, a gene expression profiling data measurement, an histology data measurement, a phenotype data measurement, or a proteomics data measurement.

44. The system of claim 39, wherein the icon is representative of a single metabolite.

45. The system of claim 39, wherein the icon is representative of a single gene.

46. The system of claim 39, wherein the icon is representative of a single gene and all icons representative of genes pertaining to a single enzyme are displayed in a vertically stacked orientation.

47. The system of claim 46, wherein iconic placement in the stack is determined by directionality and magnitude of change as compared to a standard.

48. The system of claim 39, wherein icons representative of two or more data types are displayed simultaneously.

49. The system of claim 41, wherein the interaction between the data source and the iconic display is dynamic.

50. A computer-implemented system for displaying biological sample data, wherein the data are displayed in a biological context comprising:

   a) means for providing an icon representative of a single data measurement;

   b) means for shading the icon with color, wherein color hue indicates directionality of change relative to a standard;

   c) means for adjusting color saturation in the shaded icon when the single data measurement is changed relative to the standard, wherein amount of color indicates degree of change relative to the standard;

d) means for selecting a biological context;

e) means for displaying the biological context; and

f) means for displaying the icon generated by steps (a) through (c) singularly or with a plurality of icons generated by steps (a) through (c) in a way that is representative of a relationship between the icon and the biological context.

51. The system of claim 50, wherein the color shading of step (b) is red, green, or gray color.

52. The system of claim 50, wherein the data measurement is stored as a numeric value in a data source.

53. The system of claim 52, wherein the data source is a database.

54. The system of claim 50, wherein the data measurement is selected from the group consisting of a biochemical profiling data measurement, a gene expression profiling data measurement, an histology data measurement, a phenotype data measurement, or a proteomics data measurement.

55. The system of claim 50, wherein the icon is representative of a single metabolite.

56. The system of claim 50, wherein the icon is representative of a single gene.

57. The system of claim 50, wherein the icon is representative of a single gene and all icons representative of genes pertaining to a single enzyme are displayed in a vertically stacked orientation.

58. The system of claim 57, wherein iconic placement in the stack is determined by directionality and magnitude of change as compared to a standard.

59. The system of claim 50, wherein icons representative of two or more data types are displayed simultaneously.

60. The system of claim 50, wherein the biological context is stored as alphanumeric values in a data source.

61. The system of claim 60, wherein the data source is a database.

62. The system of claim 50, wherein the biological context is represented as a graphical display.

63. The system of claim 62, wherein the graphical display type is selected from the group consisting of hierarchical, organic, circular, and orthogonal.

64. The system of claim 50, wherein the biological context is a biochemical network.

65. The system of claim 52, wherein the interaction between the data source and the iconic display is dynamic.

66. The system of claim 60, wherein the interaction between the data source and the display of the biological context is dynamic.

67. A computer-implemented system for supplying a biological context in which to display biological data comprising:

    a) means for providing at least one biological context stored as a set of alphanumeric values in a data source;

    b) means for providing at least one type of graphical display of the biological context, wherein the interaction between the data source and the graphical display is dynamic;

    c) means for selecting one biological context type for display;

    d) means for providing at least one icon representative of at least one biological data measurement;

   e) means for displaying the icon with the biological context in a way that is representative of a relationship between the icon and the biological context; and

   f) means for optionally repeating steps (c) through (e).

68. The system of claim 67, wherein the data source is a database.

69. The system of claim 67, wherein the data measurement is selected from the group consisting of a biochemical profiling data measurement, a gene expression profiling data measurement, an histology data measurement, a phenotype data measurement, or a proteomics data measurement.

70. The system of claim 67, wherein the icon is representative of a single metabolite.

71. The system of claim 67, wherein the icon is representative of a single gene.

72. The system of claim 50, wherein the icon is representative of a single gene and all icons representative of genes pertaining to a single enzyme are displayed in a vertically stacked orientation.

73. The system of claim 72, wherein iconic placement in the stack is determined by directionality and magnitude of change as compared to a standard.

74. The system of claim 67, wherein icons representative of two or more data types are displayed simultaneously.

75. The system of claim 67, wherein the graphical display type is selected from the group consisting of hierarchical, organic, circular, and orthogonal.

76. The system of claim 67, wherein the biological context is a biochemical network.